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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/724,273

DATE: 08/27/2004

TIME: 11:48:30

Input Set : N:\Crf3\RULE60\10724273.raw
 Output Set: N:\CRF4\08272004\J724273.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Palese, Peter
 6 O'Neill, Robert

8 (ii) TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL
 9 COMPOUNDS THAT INHIBIT INTERACTION OF HOST CELL PROTEINS
 10 AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

12 (iii) NUMBER OF SEQUENCES: 20

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Pennie & Edmonds
 16 (B) STREET: 1155 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: USA
 20 (F) ZIP: 10036-2711

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US/10/724,273
 30 (B) FILING DATE: 24-Nov-2003
 31 (C) CLASSIFICATION: 514

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/444,994
 34 (B) FILING DATE: 19-MAY-1995

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Coruzzi, Laura A.
 37 (B) REGISTRATION NUMBER: 30,742
 38 (C) REFERENCE/DOCKET NUMBER: 6923-054

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (212) 790-9090
 42 (B) TELEFAX: (212) 869-9741/8864
 43 (C) TELEX: 66141 PENNIE

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 19 base pairs
 50 (B) TYPE: nucleic acid
 51 (C) STRANDEDNESS: single
 52 (D) TOPOLOGY: linear

W--> 54 (ii) MOLECULE TYPE: DNA

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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61 GCAAAGCAGG AGAAACCAC

19

63 (2) INFORMATION FOR SEQ ID NO: 2:

65 (i) SEQUENCE CHARACTERISTICS:
 66 (A) LENGTH: 24 base pairs
 67 (B) TYPE: nucleic acid
 68 (C) STRANDEDNESS: single
 69 (D) TOPOLOGY: linear

W--> 71 (ii) MOLECULE TYPE: DNA

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

78 GGGTCCATCT GATAGATATG AGAG

24

80 (2) INFORMATION FOR SEQ ID NO: 3:

82 (i) SEQUENCE CHARACTERISTICS:
 83 (A) LENGTH: 48 base pairs
 84 (B) TYPE: nucleic acid
 85 (C) STRANDEDNESS: single
 86 (D) TOPOLOGY: linear

W--> 88 (ii) MOLECULE TYPE: DNA

91 (ix) FEATURE:

92 (A) NAME/KEY: modified_base
 93 (B) LOCATION: 36
 94 (D) OTHER INFORMATION: /mod_base= i

96 (ix) FEATURE:

97 (A) NAME/KEY: modified_base
 98 (B) LOCATION: 37
 99 (D) OTHER INFORMATION: /mod_base= i

101 (ix) FEATURE:

102 (A) NAME/KEY: modified_base
 103 (B) LOCATION: 41
 104 (D) OTHER INFORMATION: /mod_base= i

106 (ix) FEATURE:

107 (A) NAME/KEY: modified_base
 108 (B) LOCATION: 42
 109 (D) OTHER INFORMATION: /mod_base= i

111 (ix) FEATURE:

112 (A) NAME/KEY: modified_base
 113 (B) LOCATION: 46
 114 (D) OTHER INFORMATION: /mod_base= i

116 (ix) FEATURE:

117 (A) NAME/KEY: modified_base
 118 (B) LOCATION: 47
 119 (D) OTHER INFORMATION: /mod_base= i

122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

124 CUACUACUAC UAGGCCACGC GTCGACTACT ACGGGNNNGGG NNNGGNNG

48

126 (2) INFORMATION FOR SEQ ID NO: 4:

128 (i) SEQUENCE CHARACTERISTICS:
 129 (A) LENGTH: 20 base pairs
 130 (B) TYPE: nucleic acid
 131 (C) STRANDEDNESS: single
 132 (D) TOPOLOGY: linear

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W--> 134 (ii) MOLECULE TYPE: DNA
139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
141 TCCTGATGTT GCTGTAGACG 20
143 (2) INFORMATION FOR SEQ ID NO: 5:
145 (i) SEQUENCE CHARACTERISTICS:
146 (A) LENGTH: 20 base pairs
147 (B) TYPE: nucleic acid
148 (C) STRANDEDNESS: single
149 (D) TOPOLOGY: linear
W--> 151 (ii) MOLECULE TYPE: DNA
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
158 GCACGACTAG TATGATTG 20
160 (2) INFORMATION FOR SEQ ID NO: 6:
162 (i) SEQUENCE CHARACTERISTICS:
163 (A) LENGTH: 8 amino acids
164 (B) TYPE: amino acid
165 (C) STRANDEDNESS:
166 (D) TOPOLOGY: unknown
168 (ii) MOLECULE TYPE: peptide
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
175 Thr Gly Ala Gly Ala Gly Leu Gly
176 1 5
178 (2) INFORMATION FOR SEQ ID NO: 7:
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 5 amino acids
182 (B) TYPE: amino acid
183 (C) STRANDEDNESS:
184 (D) TOPOLOGY: unknown
186 (ii) MOLECULE TYPE: peptide
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
193 Tyr Ser Ala Ala Lys
194 1 5
196 (2) INFORMATION FOR SEQ ID NO: 8:
198 (i) SEQUENCE CHARACTERISTICS:
199 (A) LENGTH: 27 base pairs
200 (B) TYPE: nucleic acid
201 (C) STRANDEDNESS: single
202 (D) TOPOLOGY: unknown
W--> 204 (ii) MOLECULE TYPE: DNA
207 (ix) FEATURE:
208 (A) NAME/KEY: CDS
209 (B) LOCATION: 1..27
212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
214 GAC TGG CTG GAA TTC CCC ATG GCG TCC 27
215 Asp Trp Leu Glu Phe Pro Met Ala Ser
216 1 5
219 (2) INFORMATION FOR SEQ ID NO: 9:
221 (i) SEQUENCE CHARACTERISTICS:
222 (A) LENGTH: 9 amino acids

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223 (B) TYPE: amino acid
224 (D) TOPOLOGY: linear
226 (ii) MOLECULE TYPE: protein
228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
230 Asp Trp Leu Glu Phe Pro Met Ala Ser
231 1 5
233 (2) INFORMATION FOR SEQ ID NO: 10:
235 (i) SEQUENCE CHARACTERISTICS:
236 (A) LENGTH: 2940 base pairs
237 (B) TYPE: nucleic acid
238 (C) STRANDEDNESS: unknown
239 (D) TOPOLOGY: unknown
241 (ii) MOLECULE TYPE: cDNA
244 (ix) FEATURE:
245 (A) NAME/KEY: CDS
246 (B) LOCATION: 47..1663
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
251 CTAACCTTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAAT ATG ACC ACC 55
252 Met Thr Thr
253 1
255 CCA GGA AAA GAG AAC TTT CGC CTG AAA AGT TAC AAG AAC AAA TCT CTG 103
256 Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn Lys Ser Leu
257 5 10 15
259 AAT CCC GAT GAG ATG CGC AGG AGG GAG GAA GAA GGA CTG CAG TTA 151
260 Asn Pro Asp Glu Met Arg Arg Arg Glu Glu Glu Gly Leu Gln Leu
261 20 25 30 35
263 CGA AAG CAG AAA AGA GAA GAG CAG TTA TTC AAG CGG AGA AAT GTT GCT 199
264 Arg Lys Gln Lys Arg Glu Glu Gln Leu Phe Lys Arg Arg Asn Val Ala
265 40 45 50
267 ACA GCA GAA GAA ACA GAA GAA GAA GTT ATG TCA GAT GGA GGC TTT 247
268 Thr Ala Glu Glu Glu Thr Glu Glu Val Met Ser Asp Gly Gly Phe
269 55 60 65
271 CAT GAG GCT CAG ATT AGT AAC ATG GAG ATG GCA CCA GGT GGT GTC ATC 295
272 His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly Gly Val Ile
273 70 75 80
275 ACT TCT GAC ATG ATT GAG ATG ATA TTT TCC AAA AGC CCA GAG CAA CAG 343
276 Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro Glu Gln Gln
277 85 90 95
279 CTT TCA GCA ACA CAG AAA TTC AGG AAG CTG CTT TCA AAA GAA CCT AAC 391
280 Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys Glu Pro Asn
281 100 105 110 115
283 CCT CCT ATT GAT GAA GTT ATC AGC ACA CCA GGA GTA GTG GCC AGG TTT 439
284 Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val Ala Arg Phe
285 120 125 130
287 GTG GAG TTC CTC AAA CGA AAA GAG AAT TGT TCA CTG CAG TTT GAA TCA 487
288 Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln Phe Glu Ser
289 135 140 145
291 GCT TGG GTA CTG ACA AAT ATT GCT TCA GGA AAT TCT CTT CAG ACC CGA 535
292 Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu Gln Thr Arg

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293	150	155	160	
295	ATT GTG ATT CAG GCA AGA GCT GTG CCC ATC TTC ATA GAG TTG CTC AGC			583
296	Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu Leu Leu Ser			
297	165	170	175	
299	TCA GAG TTT GAA GAT GTC CAG GAA CAG GCA GTC TGG GCT CTT GGC AAC			631
300	Ser Glu Phe Glu Asp Val Gln Glu Gln Ala Val Trp Ala Leu Gly Asn			
301	180	185	190	195
303	ATT GCT GGA GAT AGT ACC ATG TGC AGG GAC TAT GTC TTA GAC TGC AAT			679
304	Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu Asp Cys Asn			
305	200	205	210	
307	ATC CTT CCC CCT CTT TTG CAG TTA TTT TCA AAG CAA AAC CGC CTG ACC			727
308	Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn Arg Leu Thr			
309	215	220	225	
311	ATG ACC CGG AAT GCA GTA TGG GCT TTG TCT AAT CTC TGT AGA GGG AAA			775
312	Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys Arg Gly Lys			
313	230	235	240	
315	AGT CCA CCT CCA GAA TTT GCA AAG GTT TCT CCA TGT CTG AAT GTG CTT			823
316	Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu Asn Val Leu			
317	245	250	255	
319	TCC TGG TTG CTG TTT GTC AGT GAC ACT GAT GTA CTG GCT GAT GCC TGC			871
320	Ser Trp Leu Leu Phe Val Ser Asp Thr Asp Val Leu Ala Asp Ala Cys			
321	260	265	270	275
323	TGG GCC CTC TCA TAT CTA TCA GAT GGA CCC AAT GAT AAA ATT CAA GCG			919
324	Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys Ile Gln Ala			
325	280	285	290	
327	GTC ATC GAT GCG GGA GTA TGT AGG AGA CTT GTG GAA CTG CTG ATG CAT			967
328	Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu Leu Met His			
329	295	300	305	
331	AAT GAT TAT AAA GTG GTT TCT CCT GCT TTG CGA GCT GTG GGA AAC ATT			1015
332	Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val Gly Asn Ile			
333	310	315	320	
335	GTC ACA GGG GAT GAT ATT CAG ACA CAG GTA ATT CTG AAT TGC TCA GCT			1063
336	Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn Cys Ser Ala			
337	325	330	335	
339	CTG CAG AGT TTA TTG CAT TTG CTG AGT AGC CCA AAG GAA TCT ATC AAA			1111
340	Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu Ser Ile Lys			
341	340	345	350	355
343	AAG GAA GCA TGT TGG ACG ATA TCT AAT ATT ACA GCT GGA AAT AGG GCA			1159
344	Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly Asn Arg Ala			
345	360	365	370	
347	CAG ATC CAG ACT GTG ATA GAT GCC AAC ATT TTC CCA GCC CTC ATT AGT			1207
348	Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala Leu Ile Ser			
349	375	380	385	
351	ATT TTA CAA ACT GCT GAA TTT CGG ACA AGA AAA GAA GCA GCT TGG GCC			1255
352	Ile Leu Gln Thr Ala Glu Phe Arg Thr Arg Lys Glu Ala Ala Trp Ala			
353	390	395	400	
355	ATC ACA AAT GCA ACT TCT GGA GGA TCA GCT GAA CAG ATC AAG TAC CTA			1303
356	Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile Lys Tyr Leu			
357	405	410	415	

VERIFICATION SUMMARY

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DATE: 08/27/2004

TIME: 11:48:31

Input Set : N:\Crf3\RULE60\10724273.raw

Output Set: N:\CRF4\08272004\J724273.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:54 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:88 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:134 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:151 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:204 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:672 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:942 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:967 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:990 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:1019 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19